

SEQUENCE LISTING



<110> Lingappa, Jaisri

5 Lingappa, Vishwanath

<120> HIV Capsid Assembly Associated Compositions and Methods

<130> UCSF.002.01US

10

<140> US 10/040,206

<141> 2002-01-02

<150> US 60/039,309

15 <151> 1997-02-07

a /<150> US 09/020,144

<151> 1998-02-06

20 <160> 6

<210> 1

<211> 1610

<212> DNA

25 <213> HIV

<220>

<223> DNA coding sequence for HIV capsid protein Pr55

30 <400> 1

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TTAAGGCCAG GGGGAAAGAA AAAATATAAG TTAAAACATA TAGTATGGC AAGCAGGGAG	120
CTAGAACGAT TCGCAGTCAA TCCTGGCCTG TTAGAACAT CAGAAGGCTG CAGACAAATA	180
35 TTGGGACAGC TACAGCCATC CCTTCAGACA GGATCAGAAG AACCTAGATC ATTATATAAT	240
ACAGTAGCAA CCCTCTATTG TGTACATCAA AGGATAGATG TAAAAGACAC CAAGGAAGCT	300
TTAGAGAAGA TAGAGGAAGA GCAAAACAAA AGTAAGAAAA AGGCACAGCA AGCAGCAGCT	360
GCAGCTGGCA CAGGAAACAG CAGCCAGGTC AGCCAAATT ACCCTATAGT GCAGAACCTA	420
CAGGGGCAAA TGGTACATCA GGCCATATCA CCTAGAACTT TAAATGCATG GGTAAAAGTA	480
40 GTAGAAGAAA AGGCTTCAG CCCAGAAGTA ATACCCATGT TTTCAGCATT ATCAGAAGGA	540
GCCACCCAC AAGATTTAAA CACCATGCTA AACACAGTGG GGGGACATCA AGCAGCCATG	600

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CAAATGTTAA AAGAGACTAT CAATGAGGAA GCTGCAGAAT GGGATAGAGT GCATCCAGTG 660
CATGCAGGGC CTATTGCACC AGGCCAAATG AGAGAACCAA GGGGAAGTGA CATAGCAGGA 720
ACTACTAGTA CCCTTCAGGA ACAAAATAGGA TGGATGACAA ATAATCCACC TATCCCAGTA 780

5 GGAGAAATCT ATAAAAGATG GATAATCCTG GGATTAATAA AAATAGTAAG AATGTATAGC 840
CCTACCAGCA TTCTGGACAT AAGACAAGGA CCAAAGGAAC CCTTTAGAGA TTATGTAGAC 900
CGGTTCTATA AAACTCTAAG AGCCGAACAA GCTTCACAGG ATGTAAAAAA TTGGATGACA 960
GAAACCTTGT TGGTCCAAAA TGCAAACCCA GATTGTAAGA CTATTTAAA AGCATTGGGA 1020
CCAGCAGCTA CACTAGAAGA AATGATGACA GCATGTCAGG GAGTGGGGGG ACCCGGCCAT 1080

10 AAAGCAAGAG TTTTGGCTGA AGCCATGAGC CAAGTAACAA ATCCAGCTAA CATAATGATG 1140
CAGAGAGGCA ATTTTAGGAA CCAAAGAAAG ACTGTTAAGT GTTCAATTG TGGCAAAGAA 1200
GGGCACATAG CCAAAAATTG CAGGGCCCT AGGAAAAAAGG GCTGTTGGAG ATGTGGAAGG 1260
GAAGGACACC AAATGAAAGA TTGCACTGAG AGACAGGCTA ATTTTTAGG GAAGATCTGG 1320
CCTTCCTACA AGGGAAGGCC AGGGAATTTC CTTCAGAGCA GACCAGAGCC AACAGCCCCA 1380

15 CCAGAAGAGA GCTTCAGGTT TGGGGAGGAG AAAACAACTC CCTCTCAGAA GCAGGAGCCG 1440
ATAGACAAGG AACTGTATCC TTAACTTCC CTCAGATCAC TCTTTGGCAA CGACCCCTCG 1500
TCACAATAAG GATAAGGGGG CAACTAAAGG AAGCTCTATT AGATACAGGA GCAGATGATA 1560
CAGTATTAGA AGAAATGAAT TTGCCAGGAA AATGGAAACC AAAAATGATA 1610

20 <210> 2
<211> 24
<212> PRT
<213> Triticum aestivum

25 | <220>
| <223> peptide fragment of host cell (wheat germ) protein HP68

<400> 2

30 Pro Arg Pro Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala Arg Val
1 5 10 15
Ile Arg Ser Leu Leu Arg Ser Asn
20

35 <210> 3
<211> 44
<212> DNA
<213> Artificial Sequence

40 <220>
<223> Degenerate oligonucleotide C-terminal peptide sequence of WGHP68

<400> .3

5 ATGAATTAC TGGGACTGCG GATAGATTAC TGGTACTGGG GATC 44

<210> 4

<211> 42

<212> DNA

10 <213> Artificial Sequence

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<223> Degenerate oligonucleotide C-terminal peptide sequence of WGHP68

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ATGAATTAC TGGGCTCTGA TAGATTACTG GTACTGGGA TC 42

<210> 5

20 <211> Length:604

<212> PRT

<213> Triticum aestivum

a /
<400> 5

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Met Ala Asp Arg Leu Thr Arg Ile Ala Ile Val Ser Glu Asp Lys Cys

1 5 10 15

Lys Pro Lys Lys Cys Arg Gln Glu Cys Lys Ser Cys Pro Val Val

20 25 30

30 Lys Thr Gly Lys Leu Cys Ile Glu Val Ser Pro Val Ala Lys Leu Ala

35 40 45

Phe Ile Ser Glu Glu Leu Cys Ile Gly Cys Gly Ile Cys Val Lys Lys

50 55 60

Cys Pro Phe Asp Ala Ile Glu Ile Ile Asn Leu Pro Lys Asp Leu Glu

35 65 70 75 80

Lys Asp Thr Thr His Arg Tyr Gly Pro Asn Thr Phe Lys Leu His Arg

85 90 95

Leu Pro Val Pro Arg Pro Gly Gln Val Leu Gly Leu Val Gly Thr Asn

100 105 110

40 Gly Ile Gly Lys Ser Thr Ala Leu Lys Val Leu Ala Gly Lys Leu Lys

115 120 125

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Pro Asn Leu Gly Arg Phe Lys Asn Pro Pro Asp Trp Gln Glu Ile Leu
130 135 140

Thr Tyr Phe Arg Gly Ser Glu Leu Gln Asn Tyr Phe Thr Arg Ile Leu

5 145 150 155 160

Glu Asp Asn Leu Lys Ala Ile Ile Lys Pro Gln Tyr Val Asp His Ile
165 170 175

Pro Lys Ala Val Gln Gly Asn Val Gly Gln Val Leu Glu Gln Lys Asp
180 185 190

10 Glu Arg Asp Met Lys Asn Glu Leu Cys Val Asp Leu Glu Leu Asn Gln
195 200 205

Val Ile Asp Arg Asn Val Gly Asp Leu Ser Gly Gly Glu Leu Gln Arg
210 215 220

Phe Ala Ile Ala Val Val Ala Val Gln Ser Ala Glu Ile Tyr Met Phe

15 225 230 235 240

Asp Glu Pro Ser Ser Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala
245 250 255

Arg Val Ile Arg Ser Leu Leu Arg Ser Asn Ser Tyr Val Ile Val Val
260 265 270

20 Glu His Asp Leu Ser Val Leu Asp Tyr Leu Ser Asp Phe Ile Cys Cys
275 280 285

Leu Tyr Gly Lys Pro Gly Ala Tyr Gly Val Val Thr Leu Pro Phe Ser
290 295 300

Val Arg Glu Gly Ile Asn Ile Phe Leu Ala Gly Phe Val Pro Thr Glu

25 305 310 315 320

Asn Leu Arg Phe Arg Asp Glu Ser Leu Thr Phe Lys Ile Ala Glu Thr
325 330 335

Gln Glu Ser Ala Glu Glu Val Ala Thr Tyr Gln Arg Tyr Lys Tyr Pro
340 345 350

30 Thr Met Ser Lys Thr Gln Gly Asn Phe Lys Leu Ser Val Val Glu Gly
355 360 365

Glu Phe Thr Asp Ser Gln Ile Val Val Met Leu Gly Glu Asn Gly Thr
370 375 380

Gly Lys Thr Thr Phe Ile Arg Met Leu Ala Gly Leu Leu Lys Pro Asp

35 385 390 395 400

Thr Met Glu Gly Thr Glu Val Glu Ile Pro Glu Phe Asn Val Ser Tyr
405 410 415

Lys Pro Gln Lys Ile Ser Pro Lys Phe Gln His Pro Val Arg His Leu
420 425 430

40 Leu His Ser Lys Ile Arg Asp Ser Tyr Thr His Pro Gln Phe Val Ser
435 440 445

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Asp Val Met Lys Pro Leu Gln Ile Glu Gln Leu Met Asp Gln Glu Val
450 455 460
Ile Asn Leu Ser Gly Gly Glu Leu Gln Arg Val Ala Leu Cys Leu Cys

5 465 470 475 480
Leu Gly Lys Pro Ala Asp Ile Tyr Leu Ile Asp Glu Pro Ser Ala Tyr
485 490 495
Leu Asp Ser Glu Gln Arg Ile Val Ala Ser Lys Val Ile Lys Arg Phe
500 505 510
10 Ile Leu His Ala Lys Lys Thr Ala Phe Ile Val Glu His Asp Phe Ile
515 520 525
Met Ala Thr Tyr Leu Ala Asp Lys Val Ile Val Tyr Glu Gly Leu Ala
530 535 540
Ser Ile Asp Cys Thr Ala Asn Ala Pro Gln Ser Leu Val Ser Gly Met
15 545 550 555 560
Asn Lys Phe Leu Ser His Leu Asp Ile Thr Phe Arg Arg Asp Pro Thr
565 570 575
Asn Tyr Arg Pro Arg Ile Asn Lys Leu Glu Ser Thr Lys Asp Arg Glu
580 585 590
20 Gln Lys Asn Ala Gly Ser Tyr Tyr Tyr Leu Asp Asp
595 600

CH1

<210> 6
<211> 599

25 <212> PRT
<213> Homo sapiens

<400> 6

30 Met Ala Asp Lys Leu Thr Arg Ile Ala Ile Val Asn His Asp Lys Cys
1 5 10 15
Lys Pro Lys Lys Cys Arg Gln Glu Cys Lys Ser Cys Pro Val Val
20 25 30
Arg Met Gly Lys Leu Cys Ile Glu Val Thr Pro Gln Ser Lys Ile Ala
35 35 40 45
Trp Ile Ser Glu Thr Leu Cys Ile Gly Cys Gly Ile Cys Ile Lys Lys
50 55 60
Cys Pro Phe Gly Ala Leu Ser Ile Val Asn Leu Pro Ser Asn Leu Glu
65 70 75 80
40 Lys Glu Thr Thr His Arg Tyr Cys Ala Asn Ala Phe Lys Leu His Arg
85 90 95

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Leu Pro Ile Pro Arg Pro Gly Glu Val Leu Gly Leu Val Gly Thr Asn
100 105 110
Gly Ile Gly Lys Ser Ala Ala Leu Lys Ile Leu Ala Gly Lys Gln Lys

5 115 120 125
Pro Asn Leu Gly Lys Tyr Asp Asp Pro Pro Asp Trp Gln Glu Ile Leu
130 135 140
Thr Tyr Phe Arg Gly Ser Glu Leu Gln Asn Tyr Phe Thr Lys Ile Leu
145 150 155 160
10 Glu Asp Asp Leu Lys Ala Ile Ile Lys Pro Gln Tyr Val Ala Arg Phe
165 170 175
Leu Arg Leu Ala Lys Gly Thr Val Gly Ser Ile Leu Asp Arg Lys Asp
180 185 190
Glu Thr Lys Thr Gln Ala Ile Val Cys Gln Gln Leu Asp Leu Thr His
15 195 200 205
Leu Lys Glu Arg Asn Val Glu Asp Leu Ser Gly Gly Glu Leu Gln Arg
210 215 220
Phe Ala Cys Ala Val Val Cys Ile Gln Lys Ala Asp Ile Phe Met Phe
225 230 235 240
20 Asp Glu Pro Ser Ser Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala
245 250 255
Ile Thr Ile Arg Ser Leu Ile Asn Pro Asp Arg Tyr Ile Ile Val Val
260 265 270
Glu His Asp Leu Ser Val Leu Asp Tyr Leu Ser Asp Phe Ile Cys Cys
25 275 280 285
Leu Tyr Gly Val Pro Ser Ala Tyr Gly Val Val Thr Met Pro Phe Ser
290 295 300
Val Arg Glu Gly Ile Asn Ile Phe Leu Asp Gly Tyr Val Pro Thr Glu
305 310 315 320
30 Asn Leu Arg Phe Arg Asp Ala Ser Leu Val Phe Lys Val Ala Glu Thr
325 330 335
Ala Asn Glu Glu Val Lys Lys Met Cys Met Tyr Lys Tyr Pro Gly
340 345 350
Met Lys Lys Met Gly Glu Phe Glu Leu Ala Ile Val Ala Gly Glu
35 355 360 365
Phe Thr Asp Ser Glu Ile Met Val Met Leu Gly Glu Asn Gly Thr Gly
370 375 380
Lys Thr Thr Phe Ile Arg Met Leu Ala Gly Arg Leu Lys Pro Asp Glu
385 390 395 400
40 Gly Gly Glu Val Pro Val Leu Asn Val Ser Tyr Lys Pro Gln Lys Ile
405 410 415

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Ser Pro Lys Ser Thr Gly Ser Val Arg Gln Leu Leu His Glu Lys Ile

420

425

430

Arg Asp Ala Tyr Thr His Pro Gln Phe Val Thr Asp Val Met Lys Pro

5 435

440

445

Leu Gln Ile Glu Asn Ile Ile Asp Gln Glu Val Gln Thr Leu Ser Gly

450

455

460

Gly Glu Leu Gln Arg Val Arg Leu Arg Leu Cys Leu Gly Lys Pro Ala

465

470

475

480

10 Asp Val Tyr Leu Ile Asp Glu Pro Ser Ala Tyr Leu Asp Ser Glu Gln

485

490

495

Arg Leu Met Ala Ala Arg Val Val Lys Arg Phe Ile Leu His Ala Lys

500

505

510

Lys Thr Ala Phe Val Val Glu His Asp Phe Ile Met Ala Thr Tyr Leu

15 515

520

525

Ala Asp Arg Val Ile Val Phe Asp Gly Val Pro Ser Lys Asn Thr Val

530

535

540

Ala Asn Ser Pro Gln Thr Leu Leu Ala Gly Met Asn Lys Phe Leu Ser

545

550

555

560

Gln Leu Glu Ile Thr Phe Arg Arg Asp Pro Asn Asn Tyr Arg Pro Arg

565

570

575

Ile Asn Lys Leu Asn Ser Ile Lys Asp Val Glu Gln Lys Lys Ser Gly

580

585

590

Asn Tyr Phe Phe Leu Asp Asp

25 595

30

35

40